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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/208,629DATE: 12/10/2000
TIME: 03:01:30

INPUT SET: S36189.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2
3 (1) General Information
4
5 (i) APPLICANT: Coughlin, Shaun R.
6 Ishihari, Hiroaki
7 Connolly, Andrew
8
9 (ii) TITLE OF THE INVENTION: Protease-Activated Receptor
10 3 and Uses Thereof
11
12 (iii) NUMBER OF SEQUENCES: 23 p. 3
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: MORRISON & FOERSTER
16 (B) STREET: 755 Page Mill Road
17 (C) CITY: Palo Alto
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 94304-1018
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Diskette
24 (B) COMPUTER: IBM Compatible
25 (C) OPERATING SYSTEM: DOS
26 (D) SOFTWARE: FastSEQ for Windows Version 2.0
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: 09/208,629
30 (B) FILING DATE: 08-DEC-1998
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 08/742,440
35 (B) FILING DATE: 30-OCT-1996
36
37
38
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Catherine M. Polizzi
41 (B) REGISTRATION NUMBER: 40,130
42 (C) REFERENCE/DOCKET NUMBER: 220002060310
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: (650) 813-5600
46 (B) TELEFAX: (650) 494-0792

Does Not Comply
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47 (C) TELEX:

48

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50

(2) INFORMATION FOR SEQ ID NO:1:

51

52 (i) SEQUENCE CHARACTERISTICS:

53

(A) LENGTH: 1224 base pairs

54

(B) TYPE: nucleic acid

55

(C) STRANDEDNESS: double

56

(D) TOPOLOGY: linear

57

58

(ii) MOLECULE TYPE: cDNA

59

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

61

62	TGACTTTGTA	TACTTAACAA	CATCCTGTAG	CCGGGTCTCA	GGACATCAAG	ATGAAAATCC	60
63	TTATCTTGGT	TGCAGCTGGG	CTGCTGTTTC	TGCCAGTCAC	TGTTTGCCAA	AGTGGCATAA	120
64	ATGTTTCAGA	CAACTCAGCA	AAGCCAACCT	TAACATATTAA	GAGTTTAAAT	GGGGGTCCCC	180
65	AAAATACCTT	TGAAGAATTC	CCACTTTCTG	ACATAGAGGG	CTGGACAGGA	GCCACCACAA	240
66	CTATAAAAGC	GGAGTGTCCC	GAGGACAGTA	TTTCAACTCT	CCACGTGAAT	AATGCTACCA	300
67	TAGGATACCT	GAGAAGTTCC	TTAAGTACCC	AAGTGATACC	TGCCATCTAT	ATCCTGCTGT	360
68	TTGTGGTTGG	TGTACCATCC	AACATCGTGA	CCCTGTGGAA	ACTCTCCTTA	AGGACCAAAT	420
69	CCATCAGTCT	GGTCATCTTT	CACACCAACC	TGGCCATCGC	AGATCTCCTT	TTCTGTGTCA	480
70	CACTGCCATT	TAAGATCGCC	TACCATCTCA	ATGGCAACAA	CTGGGTATTT	GGCGAGGTCA	540
71	TGTGCCGGAT	CACCACGGTC	GTTTTCTACG	GCAACATGTA	CTGCGCTATC	CTGATCCTCA	600
72	CTTGCATGGG	CATCAACCGC	TACCTGGCCA	CGGCTCACCC	TTTCACATAC	CAGAAGCTGC	660
73	CCAAACGCAG	CTTCTCCTTG	CTCATGTGTG	GCATAGTGTG	GGTCATGGTT	TTCTTATACA	720
74	TGCTGCCCTT	TGTCATCCTG	AAGCAGGAGT	ACCACCTCGT	CCACTCAGAG	ATCACCACCT	780
75	GCCACGATGT	CGTCGACGCG	TGCGAGTCCC	CATCATCCTT	CCGATTCTAC	TACTTCGTCT	840
76	CCTTAGCATT	CTTTGGGTTC	CTCATCCCGT	TTGTGATCAT	CATCTTCTGT	TACACGACTC	900
77	TCATCCACAA	ACTTAAATCA	AAGGATCGGA	TATGGCTGGG	CTACATCAAG	GCCGTCCTCC	960
78	TCATCCTTGT	GATTTTCACA	ATTTGCTTTG	CCCCACCAA	CATCATACTC	GTAATCCACC	1020
79	ATGCCAACTA	CTACTACCAC	AATACCGACA	GCTTGTACTT	TATGTATCTT	ATTGCTCTGT	1080
80	GCCTGGGGAG	CCTGAATAGC	TGCCTAGATC	CATTCCTTTA	CTTTGTCATG	TCGAAAGTTG	1140
81	TAGATCAGCT	TAATCCTTAG	TCGGCAATGG	CAAGACCACT	TTAGAGACCA	AGGAGAGATA	1200
82	TCTGGGAAGA	CATACATGCT	TGGC				1224

83

84

(2) INFORMATION FOR SEQ ID NO:2:

85

86

(i) SEQUENCE CHARACTERISTICS:

87

(A) LENGTH: 1124 base pairs

88

(B) TYPE: nucleic acid

89

(C) STRANDEDNESS: double

90

(D) TOPOLOGY: linear

91

92

(ii) MOLECULE TYPE: Genomic DNA

93

(ix) FEATURE:

94

95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

96

97	CCATATGCTA	ATATTTCTTT	TCAATTACAG	GCATAAATGT	TTCAGACAAC	TCAGCAAAGC	60
98	CAACCTTAAC	TATTAAGAGT	TTTAATGGGG	GTCCCCAAAA	TACCTTTGAA	GAATTCNNNN	120
99	NNNTACAACT	CTCCATGTGA	ATAATGCTAC	CATGGGATAC	CTGAGAAGTT	CCTTAAGTAC	180

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100	CAAAGTGATA	CCTGCCATCT	ACATCCTGGT	GTTTGTGATT	GGTGTACCAG	CGAACATCGT	240
101	GACCTGTGG	AAACTCTCCT	CAAGGACCAA	ATCCATCTGT	CTGGTCATCT	TTACACCAA	300
102	CCTGGCCATC	GCGGATCTCC	TTTTCTGTGT	CACGCTGCCG	TTTAAGATCN	NCCTACCATC	360
103	TCAATGGCAA	CAACTGGGTA	TTTGGCGAGG	TCATGTGCCG	GATCACCACG	GTCGTTTTCT	420
104	ACGGCAACAT	GTACTGCGCT	ANNNTCTGA	TCCTCACCTG	CATGGGCATC	AACCGCTACC	480
105	TGGCCACGGC	TCACCCTTTC	ACATAACCAGA	AGCTGCCCAA	ACGCAGCTTC	TCCATGCTCA	540
106	TGTGTGGCAT	GGTGTGGGTC	ATGGTTTTCT	TATACATGCT	GCCCTTTGTC	ATCCNNNAAG	600
107	CAGGAGTACC	ACCTCGTCCA	CTCCGAGATC	ACCACCTGCC	ACGATGTCGT	CGACGCGTGC	660
108	GANTCCCCAT	CATCCTTCCG	ATTCTACTAC	TTCGTCTCCT	TAGCATTCTT	TGGGTTCCTC	720
109	ATCCCGTTTG	TGATCATCAT	CTTCTGTTAC	ACGACTCTCA	TCCACAAACT	TAAATCAAAA	780
110	GATCNGATAT	GGCTGGGCTA	CATCAAGGCC	GTCCTCCTCA	TCCTTGTGAA	TTTCACCATC	840
111	TGCTTCCCCC	CCACCAAGNN	NNNNGATATC	TGGGAAGACG	TACATGCTTG	GCTGACTTGT	900
112	GCATGGCACC	ATCAGCTCAA	TTTTTAATTT	TTTAATTTTA	ATTTAATTTA	ATTTTATGTT	960
113	TTTGAGACAG	AGCCTCACTG	TGTAGTCCTG	GCTGGCCTGG	CTGGTTCTCT	ATTTAGACCA	1020
114	GGTTAGCCTT	GAACTCACAG	AGATCTGCCT	GCTTCTGCCT	CCCAAGTGCT	GGGTTCAACC	1080
115	AGGTCTGGCA	AGCGCTCCAT	TTTTCAGCTC	CTCTGCAACA	GTGC		1124

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
 (B) LOCATION: 5, 386, 394
 (D) OTHER INFORMATION: Xaa = stop

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Invalid Xaa

133	Thr	Leu	Tyr	Thr	Xaa	Gln	His	Pro	Val	Ala	Gly	Ser	Gln	Asp	Ile	Lys
134	1				5					10					15	
135	Met	Lys	Ile	Leu	Ile	Leu	Val	Ala	Ala	Gly	Leu	Leu	Phe	Leu	Pro	Val
136			20					25					30			
137	Thr	Val	Cys	Gln	Ser	Gly	Ile	Asn	Val	Ser	Asp	Asn	Ser	Ala	Lys	Pro
138			35				40				45					
139	Thr	Leu	Thr	Ile	Lys	Ser	Phe	Asn	Gly	Gly	Pro	Gln	Asn	Thr	Phe	Glu
140		50				55					60					
141	Glu	Phe	Pro	Leu	Ser	Asp	Ile	Glu	Gly	Trp	Thr	Gly	Ala	Thr	Thr	Thr
142	65				70				75					80		
143	Ile	Lys	Ala	Glu	Cys	Pro	Glu	Asp	Ser	Ile	Ser	Thr	Leu	His	Val	Asn
144				85				90					95			
145	Asn	Ala	Thr	Ile	Gly	Tyr	Leu	Arg	Ser	Ser	Leu	Ser	Thr	Gln	Val	Ile
146			100				105						110			
147	Pro	Ala	Ile	Tyr	Ile	Leu	Leu	Phe	Val	Val	Gly	Val	Pro	Ser	Asn	Ile
148			115				120					125				
149	Val	Thr	Leu	Trp	Lys	Leu	Ser	Leu	Arg	Thr	Lys	Ser	Ile	Ser	Leu	Val
150		130				135						140				
151	Ile	Phe	His	Thr	Asn	Leu	Ala	Ile	Ala	Asp	Leu	Phe	Cys	Val	Thr	
152	145				150					155					160	

This error appears in
Seq. 6, too.

see p. 4, too

Xaa can only represent an
amino acid. A group of
4 or more amino acidsfollowing a
stop codon
must
be shown as
a separate
sequence,
with a
different
sequence.Identification
Number, and
amino acidsalso, the response for (iii) NUMBER OF SEQUENCES: must accommodate
new sequences

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153 Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn Asn Trp Val Phe
154 165 170 175
155 Gly Glu Val Met Cys Arg Ile Thr Thr Val Val Phe Tyr Gly Asn Met
156 180 185 190
157 Tyr Cys Ala Ile Leu Ile Leu Thr Cys Met Gly Ile Asn Arg Tyr Leu
158 195 200 205
159 Ala Thr Ala His Pro Phe Thr Tyr Gln Lys Leu Pro Lys Arg Ser Phe
160 210 215 220
161 Ser Leu Leu Met Cys Gly Ile Val Trp Val Met Val Phe Leu Tyr Met
162 225 230 235 240
163 Leu Pro Phe Val Ile Leu Lys Gln Glu Tyr His Leu Val His Ser Glu
164 245 250 255
165 Ile Thr Thr Cys His Asp Val Val Asp Ala Cys Glu Ser Pro Ser Ser
166 260 265 270
167 Phe Arg Phe Tyr Tyr Phe Val Ser Leu Ala Phe Phe Gly Phe Leu Ile
168 275 280 285
169 Pro Phe Val Ile Ile Ile Phe Cys Tyr Thr Thr Leu Ile His Lys Leu
170 290 295 300
171 Lys Ser Lys Asp Arg Ile Trp Leu Gly Tyr Ile Lys Ala Val Leu Leu
172 305 310 315 320
173 Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Thr Asn Ile Ile Leu
174 325 330 335
175 Val Ile His His Ala Asn Tyr Tyr Tyr His Asn Thr Asp Ser Leu Tyr
176 340 345 350
177 Phe Met Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu Asn Ser Cys Leu
178 355 360 365
179 Asp Pro Phe Leu Tyr Phe Val Met Ser Lys Val Val Asp Gln Leu Asn
180 370 375 380
181 Pro Xaa Ser Ala Met Ala Arg Pro Leu Xaa Arg Pro Arg Arg Asp Ile
182 385 390 395 400
183 Trp Glu Asp Ile His Ala Trp
184 405
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

198	TGCTCCATGA	TTTTACAGAT	TTCATAACGT	TTAAGAGACG	GGACTCAGGT	CATCAAAATG	60
199	AAAGCCCTCA	TCTTTGCAGC	TGCTGGCCTC	CTGCTTCTGT	TGCCCACTTT	TTGTCAGAGT	120
200	GGCATGGAAA	ATGATACAAA	CAACTTGGCA	AAGCCAACCT	TACCCATTAA	GACCTTTCGT	180
201	GGAGCTCCCC	CAAATTC'TT	TGAAGAGTTC	CCCTTTTCTG	CCTTGGAAGG	CTGGACAGGA	240
202	GCCACGATTA	CTGTAAAAAT	TAAGTGCCCT	GAAGAAAGTG	CTTCACATCT	CCATGTGAAA	300
203	AATGCTACCA	TGGGGTACCT	GACCAGCTCC	TTAAGTACTA	AACTGATACC	TGCCATCTAC	360
204	CTCCTGGTGT	TTGTAGTTGG	TGTCCCGGCC	AATGCTGTGA	CCCTGTGGAT	GCTTTTCTTC	420
205	AGGACCAGAT	CCATCTGTAC	CACTGTATTC	TACACCAACC	TGGCCATTGC	AGATTTTCTT	480

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206	TTTTGTGTTA	CATTGCCCTT	TAAGATAGCT	TATCATCTCA	ATGGGAACAA	CTGGGTATTT	540
207	GGAGAGGTCC	TGTGCCGGGC	CACCACAGTC	ATCTTCTATG	GCAACATGTA	CTGCTCCATT	600
208	CTGCTCCTTG	CCTGCATCAG	CATCAACCGC	TACCTGGCCA	TCGTCCATCC	TTTCACCTAC	660
209	CGGGGCCTGC	CCAAGCACAC	CTATGCCTTG	GTAACATGTG	GACTGGTGTG	GGCAACAGTT	720
210	TTCTTATATA	TGCTGCCATT	TTTCATACTG	AAGCAGGAAT	ATTATCTTGT	TCAGCCAGAC	780
211	ATCACCACCT	GCCATGATGT	TCACAACACT	TGCGAGTCCT	CATCTCCCTT	CCAACCTCTAT	840
212	TACTTCATCT	CCTTGGCATT	CTTTGGATTG	TTAATTCAT	TTGTGCTTAT	CATCTACTGC	900
213	TATGCAGCCA	TCATCCGGAC	ACTTAATGCA	TACGATCATA	GATGGTTGTG	GTATGTTAAG	960
214	GCGAGTCTCC	TCATCCTTGT	GATTTTTTACC	ATTTGCTTTG	CTCCAAGCAA	TATTATTCTT	1020
215	ATTATTCACC	ATGCTAACTA	CTACTACAAC	AACACTGATG	GCTTATATTT	TATATATCTC	1080
216	ATAGCTTTGT	GCCTGGGTAG	TCTTAATAGT	TGCTTAGATC	CATTCCCTTA	TTTTCTCATG	1140
217	TCAAAAACCA	GAAATCACTC	CAGTGCTTAC	CTTACAAAAT	AGTGAAATGA	TCTTAGAGAA	1200
218	CAAGGACAGC	CATCACAGAG	AACG				1224

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

232	ACAGGCATGG	AAAATGATAC	AAACAACCTTG	GCAAAGCCAA	CCTTACCCAT	TAAGACCTTT	60
233	CGTGGAGCTC	CCCCAAATTC	TTTTGAAGAG	TTCCCTTTT	CTGCCTTGGA	AGGCTGGACA	120
234	GGAGCCACGA	TTACTGTAAA	AATTAAGTGC	CCTGAAGAAA	GTGCTTCACA	TCTCCATGTG	180
235	AAAAATGCTA	CCATGGGGTA	CCTGACCAGC	TCCTTAAGTA	CTAAACTGAT	ACCTGCCATC	240
236	TACCTCCTGG	TGTTTGTAGT	TGGTGTCCCG	GCCAATGCTG	TGACCCTGTG	GATGCTTTTC	300
237	TTCAGGACCA	GATCCATCTG	TACCACATGTA	TTCTACACCA	ACCTGGCCAT	TGCAGATTTT	360
238	CTTTTTTGTG	TTACATTGCC	CTTTAAGATA	GCTTATCATC	TCAATGGGAA	CAACTGGGTA	420
239	TTTGGAGAGG	TCCTGTGCCG	GGCCACCACA	GTCATCTTCT	ATGGCAACAT	GTA CTGCTCC	480
240	ATTCTGCTCC	TTGCCTGCAT	CAGCATCAAC	CGCTACCTGG	CCATCGTCCA	TCCTTTCACC	540
241	TACCGGGGCC	TGCCCAAGCA	CACCTATGCC	TTGGTAACAT	GTGGACTGGT	GTGGGCAACA	600
242	GTTTTCTTAT	ATATGCTGCC	ATTTTTTATA	CTGAAGCAGG	AATATTATCT	TGTTTCAGCCA	660
243	GACATCACCA	CCTGCCATGA	TGTTTACAAC	ACTTGCGAGT	CCTCATCTCC	CTTCCAACCTC	720
244	TATTACTTCA	TCTCCTTGGC	ATTCCTTGGG	TTCTTAATTC	CATTGTGTGCT	TATCATCTAC	780
245	TGCTATGCAG	CCATCATCCG	GACACTTAAT	GCATACGATC	ATAGATGGTT	GTGGTATGTT	840
246	AAGGCGAGTC	TCCTCATCCT	TGTGATTTTT	ACCATTTGCT	TTGCTCCAAG	CAATATTATT	900
247	CTTATTATTC	ACCATGCTAA	CTACTACTAC	AACAACACTG	ATGGCTTATA	TTTTATATAT	960
248	CTCATAGCTT	TGTGCCTGGG	TAGTCTTAAT	AGTTGCTTAG	ATCCATTCCCT	TTATTTTCTC	1020
249	ATGTCAAAAA	CCAGAAATCA	CTCCACTGCT	TACCTTACAA	AATAGTGAAA	TGATCTTAGA	1080
250	GAACAAGGAC	AGCCATCACA	GA				1102

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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SEQUENCE VERIFICATION REPORT
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